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cea ate gag ace Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr 45  ate tte cag gag tac cet gat gag ate gag tac ate tte Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe	Weber, Gunther Grimmond, Sean Nordenskjold, Magnus Larsson, Catharina  <120> A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODE SAME  <130> DAVIES  <140> 08/765,588 <141> 1996-02-22  <160> 22  <170> PatentIn Ver. 2.1  <211> 649  <212> DNA  <213> Nucleotide Sequence of VEGF165  <220> <221> CDS  <221> CDS  <221> CDS  <221> To Balance atg aac ttt ctg ctg tct tgg gtg cat tgg met Asn Phe Leu Leu Ser Trp Val His Trg for the Sequence of VEGF165  Ala Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala 15  atg gca gaa gga gga ggg cag aat cat cac gaa gtg gtg cag aag met Ala Glu Gly Gly Gln Asn His His Glu Val Val Lys 30  gat gtc tat cag cgc agc tac tgc cat cca atc gaa acc ctg Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu 50  atc ttc cag gag tac cct gat gag atc gag tac atc ttc aag Ile Phe Gln Glu Tyr Pro Asp Glu Ile 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Sean Mordenskjold, Magnus Larsson, Catharina  <120> A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING SAME  <130> DAVIES  <140> 08/765,588 <141> 1996-02-22  <160> 22  <170> PatentIn Ver. 2.1  <210> 1  <211> 649 <212> DNA <213> Nucleotide Sequence of VEGF165  <220> <221> CDS <221> CDS <221> CDS <221> CDS <221> COS <222> COS <221> COS <221> COS <221> COS <221> COS <222> COS <221> COS <221> COS <221> COS <221> COS <222> COS <221> COS <221> COS <222> COS <221> COS <221> COS <221> COS <222> COS <221> COS <221> COS <221> COS <221> COS <221> COS <222> COS <221> COS <222

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Ile	Lys 110	Pro	His	Gln	Gly	Gln 115	His	Ile	Gly	Glu	Met 120	Ser	Phe	Leu	Gln	
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Lys	Ala	Arg 175	Gln	Leu	Glu	Leu	Asn 180	Glu	Arg	Thr	Cys	Arg 185	Cys	Asp	Lys	
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as cont

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Pro Arg Glu Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln

Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly

Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys

Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg 135

Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro

Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala

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	Gln A	Arg :	Lys	Val 35	Val,	Ser	Trp	Ile	Asp 40	Val	Tyr	Thr	Arg	Ala 45	Thr	Cys	
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	Leu	Asr	n Pro	) Ası	Thi 180	Cys	s Arg	Cys	s Arg	185	s Lei 5	ı Arç	g Ar	3			
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Am. 11.																	
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Cys	Cys	Pro	Asp	Asp 85	Gly	Leu	Glu	Cys	Val 90	Pro	Thr	Gly	Gln	His 95	Gln
Val	Arg	Met	Gln 100	Ile	Leu	Met	Ile	Arg 105	Tyr	Pro	Ser	Ser	Gln 110	Leu	Gly
Glu	Met	Ser 115	Leu	Glu	Glu	His	Ser 120	Gln	Cys	Glu	Cys	Arg 125	Pro	Lys	Lys
Lys	Asp 130	Ser	Ala	Val	Lys	Pro 135	Asp	Ser	Pro	Arg	Pro 140	Leu	Cys	Pro	Arg
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Cys	Arg	Arg	Arg	Ser 165	Phe	Leu	. Arg	Cys	Gln 170	Gly	Arg	Gly	Leu	Glu 175	Leu
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															c cac
Le	ı Ala	a Pr	o Ala	a Gli 2	n Ala	a Pr	o Va	l Se	r Gl: 2	n Pr 5	o As	p Al	a Pr	o G1; 3	y His O

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Gln	Arg	Lys	Val 35	Val	Ser	Trp	Ile	Asp 40	Val	Tyr	Thr	Arg	Ala 45	Thr	Cys	
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Gly 80	Cys	Cys	Pro	Asp	Asp 85	Gly	Leu	Glu	Cys	Val 90	Pro	Thr	Gly	Gln	His 95	
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Gln	Val	Arg	Met	Gln 100	Ile	Leu	Met	Ile	Arg 105	Tyr	Pro	Ser	Ser	Gln 110	Leu	
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Gly	Glu	Met	Ser 115		Glu	Glu	His	Ser 120	Gln	. Cys	Glu	. Cys	Arg 125	Pro	Lys	
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Lys	Lys	Asp 130		.Ala	. Val	Lys	Pro 135	Asp	Arg	Cys	arg	Lys 140	Leu )	Arg	Arg	
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cca	agcto	cagg	ggag	gaat	gga g	gtact	gtct	tc ag	gttt	ctaa	c ca	ctct	gtgc	aagi	caagcat	731
ctt	cacaa	actg	gct	cttc	ctc (	ccct	cacta	aa g	aaga	ccca	a ac	ctct	gcat	aat	gggattt	791
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Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
Pro Arg Glu Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
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Pro Arg Glu Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
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Val Arg Met Gln Thr
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tgg	ata	gac	gtt	tat	gca	cgt	gcc	aca	tgc	cag	CCC	agg	gag	gtg	321
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Val	Pro 55	Leu	Ser	Met	Glu	Leu 60	Met	Gly	Asn	Val	Val 65	Lys	Gln	Leu	
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Gly									His	Gln					
ctc	atg	atc	cag	tac	ccg	agc	agt	cag	r cts	ggg	gag	atg	tcc	ctg	513
			Gln	Tyr				Glr	ı Lev					Leu	
gaa	cac	ago	caa	tgt	gaa	tgc	aga	cct	aaa	a aaa	a aag	gag	r agt	gct	561
		Ser	Glr				Arg	y Pro							
ago	r cca	gac	agg	g gtt	gcc	ata	a cc	c ca	c ca	c cg	t ccc	cag	gcc	c cgc	609
l Arg	, Pro	) Ası	) Arg	y Val	L Ala	a Ile	e Pro	o Hi	s Hi	s Ar	g Pro 145	Glr 5	n Pro	Arg	
t att			tg:	g gad	c tct	c acc	c cc	g gg	a gc	a cc	c tc	c cca	a gc	t gac	657
r Vai	l Pro	o Gly	y Tr	o Ası	o Se	r Thi	r Pr	o Gl	y Al	a Pr	o Se	r Pr	o Al	a Asp	
		t cc	c ac	t cc	a gc	c cc	a gg	a tc	c to	t gc	c cg	c ct	t gc	a ccc	705
e Il	e Hi	s Pr	o Th	r Pr	o Al	a Pr	o Gl	y Se	r Se	r Al	a Ar	g Le	u Al	a Pro 180	
	c ac	c aa	c gc	c ct	g ac	c cc	c gg	a cc	t go	c gt	t gc	c gc	t gt	a gac	753
r Al	a Al	a As	n Al	a Le	u Th	r Pr	o Gl	y Pr	ro Al	a Va	al Al	a Al	a Va	l Asp	)
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ctg gaa tgt gtg Gly Leu Glu Cys Val 90  ctc atg atc cag tac  Leu Met Ile Gln Tyr 105  agaa cac agc caa tgt 7 Glu His Ser Gln Cys 120  gagg cca gac agg gtt 1 Arg Pro Asp Arg Val 135  t gtt ccg ggc tgg gac  r Val Pro Gly Trp Asp 150  c atc cat ccc act cc e Ile His Pro Thr Pr 5  c gcc gcc aac gcc ct	cct gtg tcc cag ttt gat  Pro Val Ser Gln Phe Asp 25  tgg ata gac gtt tat gca  Trp Ile Asp Val Tyr Ala 40  gtg cct ctg agc atg gaa  Val Pro Leu Ser Met Glu 55  ccc agc tgt gtg act gtg  Pro Ser Cys Val Thr Val 70  ggc ctg gaa tgt gtg ccc Gly Leu Glu Cys Val Pro 90  ctc atg atc cag tac ccg Leu Met Ile Gln Tyr Pro 105  agaa cac agc caa tgt gaa  y Glu His Ser Gln Cys Glu 120  g agg cca gac agg gtt gcc 1 Arg Pro Asp Arg Val Ala 135  t gtt ccg ggc tgg gac tcd  r Val Pro Gly Trp Asp Sec 150  c atc cat ccc act cca gcd e Ile His Pro Thr Pro Al 5	cct gtg tcc cag ttt gat ggc Pro Val Ser Gln Phe Asp Gly tgg ata gac gtt tat gca cgt Trp Ile Asp Val Tyr Ala Arg 40 gtg cct ctg agc atg gaa ctc Val Pro Leu Ser 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Arg Val Ala Ile Pro 135  t gtt ccg ggc tgg gac tct acc ccd r Val Pro Gly Trp Asp Ser Thr Pr 150  c atc cat ccc act cca gcc cca gg e Ile His Pro Thr Pro Ala Pro Gl cc gcc gcc aac gcc ctg acc ccc gg	cct gtg tcc cag ttt gat ggc ccc agt Pro Val Ser Gln Phe Asp Gly Pro Ser 25	cet gtg tee cag ttt gat gge cee agt cae Pro Val Ser Gln Phe Asp Gly Pro Ser His agg ata gac gtt tat gea egt gee aca tge Trp Ile Asp Val Tyr Ala Arg Ala Thr Cys 40  gtg cet etg age atg gaa ete atg gge aat Val Pro Leu Ser Met Glu Leu Met Gly Asn 55  cee age tgt gtg act gtg cag ege tgt ggt Pro Ser Cys Val Thr Val Gln Arg Cys Gly gge etg gaa tgt gtg eee act ggg caa eae Gly Leu Glu Cys Val Pro Thr Gly Gln His 90  cete atg ate cag tae eeg age agt eag etg Leu Met Ile Gln Tyr Pro Ser Ser Gln Leu 110  a gaa cae age caa tgt gaa tge aga eet aaa Glu His Ser Gln Cys Glu Cys Arg Pro Lys 125  g agg cea gae agg gtt gee ata eee eae Arg Pro Asp Arg Val Ala Ile Pro His His 135  t gtt eeg gge tgg gae tet ace eeg gga ge r Val Pro Gly Trp 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 Ser
 Val
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 Trp
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Lys Lys Val Val Pro Trp Ile Asp Val Tyr Ala Arg Ala Thr Cys Gln  $$\underline{40}$$ 

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Val Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln, Arg Cys Gly Gly 65 70 75 80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln 95

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Glu Met Ser Leu Gly Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys

Lys Glu Ser Ala Val Arg Pro Asp Ser Pro Arg Ile Leu Cys Pro Pro 130

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Pro Arg Glu Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val 50 55

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly 65 70 75 80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln 85 90 95

Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly 100 105

Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys 115 120 125

Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro Arg 130 135 140,

Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg 145 150 155 160

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Arg Val Ala Ile Pro His His Arg Pro Gln Pro Arg Ser Val Pro Gly
1 10 15

Trp Asp Ser Thr Pro Gly Ala Pro Ser Pro Ala Asp Ile Ile His Pro 20 25 30

Thr Pro Ala Pro Gly Ser Ser Ala Arg Leu Ala Pro Ser Ala Ala Asn 35 40 45

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Ala Leu Thr Pro Gly Pro Ala Val Ala Ala Val Asp Ala Ala Ala Ser
                         55
Ser Ile Ala Lys Gly Gly Ala
<210> 21
<211> 71
<212> PRT
<213> hVRF186
Arg Ala Ala Thr Pro His His Arg Pro Gln Pro Arg Ser Val Pro Gly
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Trp Asp Ser Ala Pro Gly Ala Pro Ser Pro Ala Asp Ile Thr His Pro
Thr Pro Ala Pro Gly Pro Ser Ala His Ala Ala Pro Ser Thr Thr Ser
Ala Leu Thr Pro Gly Pro Ala Ala Ala Ala Ala Asp Ala Ala Ser
Ser Val Ala Lys Gly Gly Ala
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 <211> 214
 <212> PRT
 <213> mVEGF188
 Met Asn Phe Leu Leu Ser Trp Val His Trp Thr Leu Ala Leu Leu
 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Thr Thr Glu Gly
 Glu Gln Lys Ser His Glu Val Ile Lys Phe Met Asp Val Tyr Gln Arg
 Ser Tyr Cys Arg Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu Tyr
      50
 Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu Met
 Arg Cys Ala Gly Cys Cys Asn Asp Glu Ala Leu Glu Cys Val Pro Thr
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Ser Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His Gln 105



Ser Gln His Ile Gly Glu Met Ser Phe Leu Gln His Ser Arg Cys Glu 115 120 125

Cys Arg Pro Lys Lys Asp Arg Thr Lys Pro Glu Lys Lys Ser Val Arg 130 135 140

Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Lys Ser Arg Phe Lys 145 150 155

Ser Trp Ser Val His Cys Glu Pro Cys Ser Glu Arg Arg Lys His Leu 165 170 175

Phe Val Gln Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp

Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg

Cys Asp Lys Pro Arg Arg 210